SCORE Search Results Details for Application 10579500 and Search Result 20080607_135308_us-10-579-500-1.rng.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10579500 and Search Result 20080607_135308_us-10-579-500-1.rng.

Go Back to previous page

GenCore version 6.2.1
Copyright (c) 1993 - 2008 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2008, 13:55:01 ; Search time 880 Seconds
(without alignments)
895.527 Million cell updates/sec

Title: US-10-579-500-1
Perfect score: 73
Sequence: 1 cttttctgtttagtttttac.....agacccaggggagaatgggt 73

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9073515 seqs, 5397694045 residues

Total number of hits satisfying chosen parameters: 18147030

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200711:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*

9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2004c:*
15: geneseqn2004d:*
16: geneseqn2005a:*
17: geneseqn2005b:*
18: geneseqn2005c:*
19: geneseqn2006a:*
20: geneseqn2006b:*
21: geneseqn2006c:*
22: geneseqn2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	73	100.0	73	16	AEA47577	Aea47577 Nucleotid
2	73	100.0	73	19	AEG24649	Aeg24649 Mammalian
3	73	100.0	502	16	AEA47605	Aea47605 Nucleotid
4	73	100.0	540	16	AEA47599	Aea47599 Nucleotid
5	73	100.0	612	19	AEG24646	Aeg24646 Mammalian
6	73	100.0	614	13	ADR12359	Adr12359 Human Her
7	73	100.0	614	19	AEG24601	Aeg24601 Mammalian
8	73	100.0	615	16	AEA47580	Aea47580 Nucleotid
9	73	100.0	4529	12	ADJ57169	Adj57169 Human Her
10	73	100.0	4530	2	AAT01585	Aat01585 Her-2/neu
11	73	100.0	4530	2	AAT71253	Aat71253 Human HER
12	73	100.0	4530	3	AAZ60815	Aaz60815 Nucleotid
13	73	100.0	4530	5	AAD19731	Aad19731 Human tyr
14	73	100.0	4530	6	ABK83918	Abk83918 Human cDN
15	73	100.0	4530	6	ABN85585	Abn85585 Human HER
16	73	100.0	4530	6	ABV94128	Abv94128 Breast ca
17	73	100.0	4530	7	ABZ35012	Abz35012 Human gen
18	73	100.0	4530	8	ABQ83856	Abq83856 Human Her
19	73	100.0	4530	8	ACC50139	Acc50139 Breast ca
20	73	100.0	4530	8	ADC09594	Adc09594 Her2/Neu
21	73	100.0	4530	10	AAD58073	Aad58073 Human c-e
22	73	100.0	4530	12	ADH13161	Adh13161 Human mal
23	73	100.0	4530	12	ADJ32564	Adj32564 Human HER
24	73	100.0	4530	12	ADM72832	Adm72832 Human Her
25	73	100.0	4530	12	ACN40176	Acn40176 Tumour-as

26	73	100.0	4530	13	ADO20008	Ado20008 Human PRO
27	73	100.0	4530	13	ADQ29633	Adq29633 Human col
28	73	100.0	4530	13	ADR83426	Adr83426 Human hum
29	73	100.0	4530	16	ADW44364	Adw44364 Human tyr
30	73	100.0	4530	16	ADW28639	Adw28639 HER2 codi
31	73	100.0	4530	16	ADY61191	Ady61191 Breast ca
32	73	100.0	4530	16	ADZ09642	Adz09642 Human bre
33	73	100.0	4530	16	AEA15048	Aea15048 Human pol
34	73	100.0	4530	16	AEA08354	Aea08354 Human c-e
35	73	100.0	4530	19	AEE39927	Aee39927 Human HER
36	73	100.0	4530	19	AEF13909	Aef13909 Human Her
37	73	100.0	4530	19	AEF69945	Aef69945 Colorecta
38	73	100.0	4530	19	AEG47307	Aeg47307 Human col
39	73	100.0	4530	19	AEH30434	Aeh30434 Human erb
40	73	100.0	4530	19	AEI92573	Aei92573 Human Her
41	73	100.0	4530	22	AEP62395	Aep62395 Human Ner
42	73	100.0	4530	22	AGD53333	Agd53333 Human Erb
43	73	100.0	4530	22	AGE12386	Age12386 Human HER
44	73	100.0	4647	16	ADZ47802	Adz47802 DNA encod
45	73	100.0	5125	13	ADQ21799	Adq21799 Human sof

ALIGNMENTS

RESULT 1
AEA47577
ID   AEA47577 standard; DNA; 73 BP.
XX
AC   AEA47577;
XX
DT   11-AUG-2005 (first entry)
XX
DE   Nucleotide sequence of 3' her2 UTR fragment TRE1.
XX
KW   gene expression; untranslated region; UTR; her2;
KW   translational regulatory element; TRE; ss.
XX
OS   Synthetic.
XX
PN   WO2005049868-A1.
XX
PD   02-JUN-2005.
XX
PF   17-NOV-2004; 2004WO-US038496.
XX
PR   17-NOV-2003; 2003US-0520384P.
XX
PA   (PCTT-) PCT THERAPEUTICS INC.

XX
PI Mehta A, Trotta CR;
XX
DR WPI; 2005-417744/42.
XX
PT Determining whether a candidate compound modulates gene expression by
PT providing a compound and a reporter gene in a system and detecting
PT expression of the reporter gene in the system.
XX
PS Claim 1; SEQ ID NO 1; 93pp; English.
XX
CC The specification describes a method of determining whether a candidate
CC compound modulates gene expression. The method comprises providing a
CC compound and a reporter gene in a system and detecting expression of the
CC reporter gene in the system. The reporter gene is linked to an
CC untranslated region (UTR) of her2. Expression of the reporter gene is
CC altered relative to expression of a reporter gene not linked to the UTR.
CC The method of the invention is useful for determining whether a candidate
CC compound modulates gene expression, screening for compounds that modulate
CC Her2 expression, and identifying a compound that modulates reporter gene
CC expression. Compounds identified using the method of the invention are
CC useful for modulating expression of Her2. The present sequence represents
CC a translational regulatory element (TRE) 1, derived from a 3' her2 UTR.
CC It is used as the UTR in the method of the invention.
XX
SQ Sequence 73 BP; 17 A; 7 C; 15 G; 34 T; 0 U; 0 Other;

  Query Match   100.0%; Score 73; DB 16; Length 73;
  Best Local Similarity   100.0%; Pred. No. 3.8e-07;
  Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db         61 GGGGAGAATGGGT 73
```

RESULT 2
AEG24649
ID AEG24649 standard; DNA; 73 BP.
XX
AC AEG24649;
XX
DT 04-MAY-2006 (first entry)
XX
DE Mammalian expression vector related DNA SEQ ID NO 116.

XX
KW Cytostatic; Antiinflammatory; Antimicrobial; Immunosuppressive;
KW Cardiovascular-Gen.; CNS-Gen.; UTR-dependent expression modulator;
KW expression vector; gene expression; diagnosis; proliferative disorder;
KW inflammation; infection; immune disorder; cardiovascular disease;
KW neurological disease; ds.
XX
OS Synthetic.
XX
PN WO2006022712-A1.
XX
PD 02-MAR-2006.
XX
PF 16-AUG-2004; 2004WO-US026309.
XX
PR 21-JUL-2004; 2004US-00895393.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Cao L, Mehta A, Naryshkin NA, Pelligrini MC, Romfo CM;
PI Trifillis P, Trotta CR;
XX
DR WPI; 2006-194058/20.
XX
PT Novel nucleic acid construct comprising high-level mammalian expression
PT vector, nucleic acid sequence encoding reporter polypeptide and
PT optionally intron, useful for screening compound that modulates
PT expression of polypeptide.
XX
PS Disclosure; SEQ ID NO 116; 150pp; English.
XX
CC The invention relates to a nucleic acid construct (I) comprising a high-
CC level mammalian expression vector, a nucleic acid sequence encoding a
CC reporter polypeptide, and optionally an intron, where the nucleic acid
CC sequence encoding a reporter polypeptide is proximally linked to a target
CC untranslated region (UTR), or directly linked to one or more target UTRs.
CC (I) or the nucleic acid is useful for screening a compound that modulates
CC expression of a polypeptide, for screening in vivo for a compound that
CC modulates UTR-dependent expression, for screening in vitro for a compound
CC that modulates UTR-affected expression, for screening for a compound that
CC modulates protein expression through a main ORF-independent, UTR-affected
CC mechanism, and for screening a compound that modulates protein expression
CC through a UTR-affected mechanism. The population of nucleic acids is
CC useful to produce polypeptides in vitro and for expressing a nucleic acid
CC molecule in a cell. (I) or the nucleic acid is useful for screening a
CC compound that modulates gene expression, or modulates mdm2 mRNA
CC translation, where the compounds are useful in diagnostic assays for
CC detecting diseases and abnormalities or susceptibility to diseases and
CC abnormalities related to the presence of mutations in the nucleic acid

```
CC   sequences that encode a gene expression modulator. The compounds
CC   identified may be used in the treatment of diseases where the target gene
CC   is overexpressed or is expressed in low levels, such as a proliferative
CC   disorder, inflammatory disorder, an infectious disease, an autoimmune
CC   disorder, a cardiovascular disorder or a CNS disorder. The present
CC   sequence represents a mammalian expression vector related DNA.
XX
SQ   Sequence 73 BP; 17 A; 7 C; 15 G; 34 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 73;  DB 19;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-07;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db         61 GGGGAGAATGGGT 73


RESULT 3
AEA47605
ID   AEA47605 standard; DNA; 502 BP.
XX
AC   AEA47605;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Nucleotide sequence of a deleted Her2 3' UTR variant.
XX
KW   gene expression; untranslated region; UTR; Her2; ss.
XX
OS   Synthetic.
XX
PN   WO2005049868-A1.
XX
PD   02-JUN-2005.
XX
PF   17-NOV-2004; 2004WO-US038496.
XX
PR   17-NOV-2003; 2003US-0520384P.
XX
PA   (PCTT-) PCT THERAPEUTICS INC.
XX
PI   Mehta A,  Trotta CR;
XX
DR   WPI; 2005-417744/42.
```

XX
PT Determining whether a candidate compound modulates gene expression by
PT providing a compound and a reporter gene in a system and detecting
PT expression of the reporter gene in the system.
XX
PS Example 5; SEQ ID NO 29; 93pp; English.
XX
CC The specification describes a method of determining whether a candidate
CC compound modulates gene expression. The method comprises providing a
CC compound and a reporter gene in a system and detecting expression of the
CC reporter gene in the system. The reporter gene is linked to an
CC untranslated region (UTR) of her2. Expression of the reporter gene is
CC altered relative to expression of a reporter gene not linked to the UTR.
CC The method of the invention is useful for determining whether a candidate
CC compound modulates gene expression, screening for compounds that modulate
CC Her2 expression, and identifying a compound that modulates reporter gene
CC expression. Compounds identified using the method of the invention are
CC useful for modulating expression of Her2. The present sequence represents
CC a Her2 3' UTR variant, with nucleotides 1-110 deleted at the 5' end.
XX
SQ Sequence 502 BP; 117 A; 116 C; 138 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 16; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 414

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db        415 GGGGAGAATGGGT 427
```

RESULT 4
AEA47599
ID AEA47599 standard; DNA; 540 BP.
XX
AC AEA47599;
XX
DT 11-AUG-2005 (first entry)
XX
DE Nucleotide sequence of a Her2 3' UTR variant.
XX
KW gene expression; untranslated region; UTR; Her2; ss.
XX
OS Synthetic.
XX

PN   WO2005049868-A1.
XX
PD   02-JUN-2005.
XX
PF   17-NOV-2004; 2004WO-US038496.
XX
PR   17-NOV-2003; 2003US-0520384P.
XX
PA   (PCTT-) PCT THERAPEUTICS INC.
XX
PI   Mehta A, Trotta CR;
XX
DR   WPI; 2005-417744/42.
XX
PT   Determining whether a candidate compound modulates gene expression by
PT   providing a compound and a reporter gene in a system and detecting
PT   expression of the reporter gene in the system.
XX
PS   Disclosure; SEQ ID NO 23; 93pp; English.
XX
CC   The specification describes a method of determining whether a candidate
CC   compound modulates gene expression. The method comprises providing a
CC   compound and a reporter gene in a system and detecting expression of the
CC   reporter gene in the system. The reporter gene is linked to an
CC   untranslated region (UTR) of her2. Expression of the reporter gene is
CC   altered relative to expression of a reporter gene not linked to the UTR.
CC   The method of the invention is useful for determining whether a candidate
CC   compound modulates gene expression, screening for compounds that modulate
CC   Her2 expression, and identifying a compound that modulates reporter gene
CC   expression. Compounds identified using the method of the invention are
CC   useful for modulating expression of Her2. The present sequence represents
CC   a Her2 3' UTR variant.
XX
SQ   Sequence 540 BP; 127 A; 132 C; 156 G; 125 T; 0 U; 0 Other;

  Query Match   100.0%; Score 73; DB 16; Length 540;
  Best Local Similarity   100.0%; Pred. No. 3.6e-07;
  Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 527

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db        528 GGGGAGAATGGGT 540
```

RESULT 5

AEG24646
ID   AEG24646 standard; DNA; 612 BP.
XX
AC   AEG24646;
XX
DT   04-MAY-2006 (first entry)
XX
DE   Mammalian expression vector related DNA SEQ ID NO 113.
XX
KW   Cytostatic; Antiinflammatory; Antimicrobial; Immunosuppressive;
KW   Cardiovascular-Gen.; CNS-Gen.; UTR-dependent expression modulator;
KW   expression vector; gene expression; diagnosis; proliferative disorder;
KW   inflammation; infection; immune disorder; cardiovascular disease;
KW   neurological disease; ds.
XX
OS   Synthetic.
XX
PN   WO2006022712-A1.
XX
PD   02-MAR-2006.
XX
PF   16-AUG-2004; 2004WO-US026309.
XX
PR   21-JUL-2004; 2004US-00895393.
XX
PA   (PTCT-) PTC THERAPEUTICS INC.
XX
PI   Cao L, Mehta A, Naryshkin NA, Pelligrini MC, Romfo CM;
PI   Trifillis P, Trotta CR;
XX
DR   WPI; 2006-194058/20.
XX
PT   Novel nucleic acid construct comprising high-level mammalian expression
PT   vector, nucleic acid sequence encoding reporter polypeptide and
PT   optionally intron, useful for screening compound that modulates
PT   expression of polypeptide.
XX
PS   Disclosure; SEQ ID NO 113; 150pp; English.
XX
CC   The invention relates to a nucleic acid construct (I) comprising a high-
CC   level mammalian expression vector, a nucleic acid sequence encoding a
CC   reporter polypeptide, and optionally an intron, where the nucleic acid
CC   sequence encoding a reporter polypeptide is proximally linked to a target
CC   untranslated region (UTR), or directly linked to one or more target UTRs.
CC   (I) or the nucleic acid is useful for screening a compound that modulates
CC   expression of a polypeptide, for screening in vivo for a compound that
CC   modulates UTR-dependent expression, for screening in vitro for a compound
CC   that modulates UTR-affected expression, for screening for a compound that
CC   modulates protein expression through a main ORF-independent, UTR-affected

CC mechanism, and for screening a compound that modulates protein expression
CC through a UTR-affected mechanism. The population of nucleic acids is
CC useful to produce polypeptides in vitro and for expressing a nucleic acid
CC molecule in a cell. (I) or the nucleic acid is useful for screening a
CC compound that modulates gene expression, or modulates mdm2 mRNA
CC translation, where the compounds are useful in diagnostic assays for
CC detecting diseases and abnormalities or susceptibility to diseases and
CC abnormalities related to the presence of mutations in the nucleic acid
CC sequences that encode a gene expression modulator. The compounds
CC identified may be used in the treatment of diseases where the target gene
CC is overexpressed or is expressed in low levels, such as a proliferative
CC disorder, inflammatory disorder, an infectious disease, an autoimmune
CC disorder, a cardiovascular disorder or a CNS disorder. The present
CC sequence represents a mammalian expression vector related DNA.
XX
SQ Sequence 612 BP; 143 A; 147 C; 175 G; 147 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 19; Length 612;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 524

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db        525 GGGGAGAATGGGT 537
```

RESULT 6
ADR12359
ID ADR12359 standard; DNA; 614 BP.
XX
AC ADR12359;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human Her2 3'-untranslated region DNA.
XX
KW ss; cytostatic; VEGF modulator; angiogenesis inhibitor;
KW UTR-dependent expression; vascular endothelial growth factor;
KW untranslated region; cancer; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO2004065561-A2.
XX
PD 05-AUG-2004.

XX
PF 21-JAN-2004; 2004WO-US001643.
XX
PR 21-JAN-2003; 2003US-0441637P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Cao L, Trifillis P;
XX
DR WPI; 2004-571681/55.
XX
PT Identifying modulators of untranslated region-dependent expression of a
PT VEGF gene, useful for treating cancer, comprises contacting a compound
PT with a cell or translation mixture containing a reporter gene linked to a
PT VEGF gene UTR.
XX
PS Example; SEQ ID NO 68; 251pp; English.
XX
CC A method of identifying (M1) a compound that modulates untranslated
CC region-dependent expression of a vascular endothelial growth factor
CC (VEGF) gene comprises contacting a member of a library of compounds with
CC a cell or cell-free translation mixture containing a reporter gene
CC operably linked to an untranslated region (UTR) of the VEGF gene, and
CC detecting expression of the reporter gene. A compound is identified as
CC modulator if the level of expression of the reporter gene in the presence
CC of the compound is altered as compared to that in the absence of the
CC compound or in the presence of a control. Compounds identified by M1 are
CC useful for treating, preventing or ameliorating cancer or its symptoms,
CC and/or for inhibiting angiogenesis. This sequence corresponds to a
CC therapeutic untranslated region used in the invention.
XX
SQ Sequence 614 BP; 144 A; 146 C; 176 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 13; Length 614;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 527

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db        528 GGGGAGAATGGGT 540
```

RESULT 7
AEG24601
ID AEG24601 standard; DNA; 614 BP.

XX
AC AEG24601;
XX
DT 04-MAY-2006 (first entry)
XX
DE Mammalian expression vector related DNA SEQ ID NO 68.
XX
KW Cytostatic; Antiinflammatory; Antimicrobial; Immunosuppressive;
KW Cardiovascular-Gen.; CNS-Gen.; UTR-dependent expression modulator;
KW expression vector; gene expression; diagnosis; proliferative disorder;
KW inflammation; infection; immune disorder; cardiovascular disease;
KW neurological disease; ds.
XX
OS Homo sapiens.
XX
PN WO2006022712-A1.
XX
PD 02-MAR-2006.
XX
PF 16-AUG-2004; 2004WO-US026309.
XX
PR 21-JUL-2004; 2004US-00895393.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Cao L, Mehta A, Naryshkin NA, Pelligrini MC, Romfo CM;
PI Trifillis P, Trotta CR;
XX
DR WPI; 2006-194058/20.
XX
PT Novel nucleic acid construct comprising high-level mammalian expression
PT vector, nucleic acid sequence encoding reporter polypeptide and
PT optionally intron, useful for screening compound that modulates
PT expression of polypeptide.
XX
PS Disclosure; SEQ ID NO 68; 150pp; English.
XX
CC The invention relates to a nucleic acid construct (I) comprising a high-
CC level mammalian expression vector, a nucleic acid sequence encoding a
CC reporter polypeptide, and optionally an intron, where the nucleic acid
CC sequence encoding a reporter polypeptide is proximally linked to a target
CC untranslated region (UTR), or directly linked to one or more target UTRs.
CC (I) or the nucleic acid is useful for screening a compound that modulates
CC expression of a polypeptide, for screening in vivo for a compound that
CC modulates UTR-dependent expression, for screening in vitro for a compound
CC that modulates UTR-affected expression, for screening for a compound that
CC modulates protein expression through a main ORF-independent, UTR-affected
CC mechanism, and for screening a compound that modulates protein expression
CC through a UTR-affected mechanism. The population of nucleic acids is

```
CC   useful to produce polypeptides in vitro and for expressing a nucleic acid
CC   molecule in a cell. (I) or the nucleic acid is useful for screening a
CC   compound that modulates gene expression, or modulates mdm2 mRNA
CC   translation, where the compounds are useful in diagnostic assays for
CC   detecting diseases and abnormalities or susceptibility to diseases and
CC   abnormalities related to the presence of mutations in the nucleic acid
CC   sequences that encode a gene expression modulator. The compounds
CC   identified may be used in the treatment of diseases where the target gene
CC   is overexpressed or is expressed in low levels, such as a proliferative
CC   disorder, inflammatory disorder, an infectious disease, an autoimmune
CC   disorder, a cardiovascular disorder or a CNS disorder. The present
CC   sequence represents a mammalian expression vector related DNA.
XX
SQ   Sequence 614 BP; 144 A; 146 C; 176 G; 148 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 73;  DB 19;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-07;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 527

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db        528 GGGGAGAATGGGT 540


RESULT 8
AEA47580
ID   AEA47580 standard; DNA; 615 BP.
XX
AC   AEA47580;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Nucleotide sequence of a fragment from a 3' her2 UTR.
XX
KW   gene expression; untranslated region; UTR; her2; ss.
XX
OS   Synthetic.
XX
PN   WO2005049868-A1.
XX
PD   02-JUN-2005.
XX
PF   17-NOV-2004; 2004WO-US038496.
XX
PR   17-NOV-2003; 2003US-0520384P.
```

XX
PA (PCTT-) PCT THERAPEUTICS INC.
XX
PI Mehta A, Trotta CR;
XX
DR WPI; 2005-417744/42.
XX
PT Determining whether a candidate compound modulates gene expression by
PT providing a compound and a reporter gene in a system and detecting
PT expression of the reporter gene in the system.
XX
PS Example 3; SEQ ID NO 4; 93pp; English.
XX
CC The specification describes a method of determining whether a candidate
CC compound modulates gene expression. The method comprises providing a
CC compound and a reporter gene in a system and detecting expression of the
CC reporter gene in the system. The reporter gene is linked to an
CC untranslated region (UTR) of her2. Expression of the reporter gene is
CC altered relative to expression of a reporter gene not linked to the UTR.
CC The method of the invention is useful for determining whether a candidate
CC compound modulates gene expression, screening for compounds that modulate
CC Her2 expression, and identifying a compound that modulates reporter gene
CC expression. Compounds identified using the method of the invention are
CC useful for modulating expression of Her2. The present sequence represents
CC a fragment from a 3' her2 UTR, which was shown to override the
CC translational repression of a reporter gene linked to AEA47581.
XX
SQ Sequence 615 BP; 144 A; 147 C; 176 G; 148 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 16; Length 615;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 527

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db        528 GGGGAGAATGGGT 540
```

RESULT 9
ADJ57169
ID ADJ57169 standard; cDNA; 4529 BP.
XX
AC ADJ57169;
XX
DT 06-MAY-2004 (first entry)

XX
DE Human Her-2/neu gene cDNA sequence.
XX
KW Her-2/neu; vaccine; cancer; glycoprotein D; cytokine; cytostatic; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004007734-A1.
XX
PD 22-JAN-2004.
XX
PF 15-JUL-2003; 2003WO-KR001400.
XX
PR 16-JUL-2002; 2002KR-00041764.
PR 12-JUN-2003; 2003KR-00038012.
XX
PA (PANG-) PANGENOMICS CO LTD.
XX
PI Lee JY, Kim D, Chung Y, Chang S, Lee K, Kang C;
XX
DR WPI; 2004-122962/12.
XX
PT New Her-2/neu plasmid construct having anti-cancer activity, useful for
PT preparing a DNA vaccine for preventing and/or treating cancer.
XX
PS Example 1; SEQ ID NO 1; 70pp; English.
XX
CC The invention relates to an Her-2/neu plasmid construct having anti-
CC cancer activity that is prepared by inserting a truncated human Her-2/neu
CC gene lacking the intracellular domain into plasmid pTV2 or pCK. Aslo
CC provided are a DNA vaccine for preventing and/or treating cancer
CC comprising the plasmid construct and a carrier; and a method for
CC preventing and/or treating cancer by administering the DNA vaccine cited
CC above. The construct is pNeuTM (KCCM-10393), pCKTM (KCCM-10396), pNeuECD
CC (KCCM-10394) or pCKECD (KCCM-10395). The truncated human Her-2/neu gene
CC further lacks the transmembrane domain. The signal peptide of the human
CC Her-2/neu gene is replaced by the signal peptide of herpes simplex type 1
CC glycoprotein D (gD). The plasmid construct is preferably pNeuTM-gDs. The
CC plasmid construct further translates a cytokine gene besides the human
CC Her-2/neu gene. The cytokine gene is selected from granulocyte-macrophage
CC colony-stimulating factor (GM-CSF), FMS-like tyrosine kinase 3 ligand
CC (Flt3L), early T lymphocyte activation-1 (Eta-1), interleukin-12 (IL-12),
CC IL-15 and IL-18. The DNA vaccine further comprises a cytokine gene
CC expressing plasmid. The Her-2/neu plasmid construct is useful for
CC preparing a DNA vaccine for treating and/or preventing cancer. The
CC present sequence represents a human Her-2/neu gene cDNA sequence.
XX
SQ Sequence 4529 BP; 921 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 73;  DB 12;  Length 4529;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-07;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4382 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 4441

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4442 GGGGAGAATGGGT 4454


RESULT 10
AAT01585
ID   AAT01585 standard; DNA; 4530 BP.
XX
AC   AAT01585;
XX
DT   20-APR-1996  (first entry)
XX
DE   Her-2/neu (ERBB2/c-erbB-2) gene sequence.
XX
KW   Her-2/neu; Erb-B2; c-erbB-2; oncogene; DNA binding protein; HPBF;
KW   Erb-B2 promoter binding protein; tumour enhancer factor;
KW   breast cancer diagnosis; prognosis; antisense oligonucleotide;
KW   retro virus vector; gene therapy vector; ss.
XX
OS   Homo sapiens.
XX
PN   WO9528485-A1.
XX
PD   26-OCT-1995.
XX
PF   19-APR-1995;   95WO-US004953.
XX
PR   19-APR-1994;   94US-00229515.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Raziuddin F,  Sarkar FH;
XX
DR   WPI; 1995-373800/48.
XX
PT   New purified protein binding to the ERBB2 gene promoter - to induce cell
PT   proliferation, diagnostic of breast cancer, also related antibodies,
PT   nucleic acid, assays and methods for screening inhibitors.
XX
```

```
PS   Disclosure; Page 52-54; 69pp; English.
XX
CC   The Erb-B2 gene is one of the primary genes responsible for the
CC   transition of normal breast epithelial cells towards carcinoma in situ
CC   and the subsequent development of invasive and metastatic cancer. HPBF
CC   (see AAR77093-94), the Erb-B2 promoter binding protein, induces cell
CC   division on binding to the promoter. In a method for greater success in
CC   early identification and treatment of breast cancer, the initation step
CC   for Erb-B2 gene activity is identified. This method involves determining
CC   the presence of HPBF in a biopsy from the subject, where the presence of
CC   HPBF (relative to its absence in a normal control) indicates the presence
CC   of cancer and a decreased chance of long-term survival. Binding of HPBF
CC   to the promoter can be inhibited using antisense oligonucleotides or a
CC   non-genomic nucleic acid that binds to HPBF; these oligos can be
CC   expressed from retro virus or other gene therapy vectors
XX
SQ   Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 73;  DB 2;  Length 4530;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-07;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4383 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTAAAGACGAAATAAAGACCCA 4442

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4443 GGGGAGAATGGGT 4455


RESULT 11
AAT71253
ID   AAT71253 standard; DNA; 4530 BP.
XX
AC   AAT71253;
XX
DT   11-JUN-2007  (revised)
DT   30-MAR-1998  (first entry)
XX
DE   Human HER2 gene.
XX
KW   HER2; cognate transgene; human; tyrosine kinase-type receptor; lymphoma;
KW   cellular immunogen; cancer; self-determinant immunoreactivity;
KW   cancer vaccination; breast carcinoma; colon carcinoma; immunotherapy;
KW   proto-oncogene; ss.
XX
OS   Homo sapiens.
XX
```

PN   WO9725860-A1.
XX
PD   24-JUL-1997.
XX
PF   13-JAN-1997;   97WO-US000582.
XX
PR   19-JAN-1996;   96US-0010262P.
XX
PA   (UYAL-) UNIV ALLEGHENY HEALTH SCI.
XX
PI   Halpern MS, England JM;
XX
DR   WPI; 1997-384993/35.
DR   PC:NCBI; gi183986.
DR   PC_ENCPRO:NCBI; gi306840.
XX
PT   Proto-oncogene immunogen - used in vaccine for the prevention and
PT   treatment of cancer.
XX
PS   Disclosure; Page 56-58; 81pp; English.
XX
CC   This sequence represents the human HER2 cognate transgene (CTG). Deletion
CC   of amino acids 1-731 of the encoded protein renders the CTG non-
CC   transforming. HER2 is a tyrosine kinase-type receptor. This sequence can
CC   be used in the cellular immunogen of the invention. The cellular
CC   immunogen of the invention is for immunising against the product of a
CC   target proto-oncogene, over-expression of which is associated with
CC   cancer, comprises host cells transfected with a construct containing at
CC   least one transgene related to the proto-oncogene and driven by a strong
CC   promoter. The product of the transgene induces immunoreactivity to host
CC   self-determinants on the product of proto-oncogene. The cellular
CC   immunogens are used for protective vaccination against cancer (e.g.
CC   carcinoma of breast or colon, or various lymphomas) and for immunotherapy
CC   of cancer. Use of the immunogen eliminates the need to isolate
CC   immunogenic, HLA host-matched peptides. The method is not based on immune
CC   recognition of a determinant defined by a cancer-specific mutation and
CC   generates a systemic (anti-metastatic) response
CC
CC   Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

  Query Match   100.0%; Score 73; DB 2; Length 4530;
  Best Local Similarity   100.0%; Pred. No. 3.3e-07;
  Matches   73; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db       4383 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 4442

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4443 GGGGAGAATGGGT 4455


RESULT 12
AAZ60815
ID   AAZ60815 standard; DNA; 4530 BP.
XX
AC   AAZ60815;
XX
DT   11-JUN-2007  (revised)
DT   16-MAY-2000  (first entry)
XX
DE   Nucleotide sequence of a cognate transgene of c-neu.
XX
KW   Cognate transgene; CTG; tumourigenic; cellular immunogen; immunisation;
KW   proto-oncogene; malignanacy; allogenic cell; vaccine; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004927-A1.
XX
PD   03-FEB-2000.
XX
PF   08-JUL-1999;   99WO-US015594.
XX
PR   24-JUL-1998;   98US-0093965P.
XX
PA   (UYAL-) UNIV ALLEGHNEY HEALTH SCI.
PA   (HALP/) HALPERN M S.
PA   (ENGL/) ENGLAND J M.
XX
PI   Halpern MS,  England JM;
XX
DR   WPI; 2000-182543/16.
DR   PC:NCBI; gi183986.
DR   PC_ENCPRO:NCBI; gi306840.
XX
PT   Cellular immunogens comprising allogenic donor cells transfected with a
PT   construct comprising a proto-oncogene cognate, useful as cancer vaccines.
XX
PS   Disclosure; Page 66-68; 77pp; English.
XX
CC   The present sequence represents a cognate transgene (CTG) which is
CC   rendered non-tumourigenic by deletion of amino acids 1-731. The CTG is
CC   used in the course of the invention. The specification describes a
```

CC cellular immunogen for immunizing a host against the effects of the
CC product of a target proto-oncogene which is associated with a
CC malignanacy. The cellular immunogen comprises allogenic cells transfected
CC with transgene construct comprising a transgene cognate to target proto-
CC oncogene and a strong promoter. The cellular immunogen is useful for
CC vaccinating a host against cancer by inserting the transgene construct
CC into the body of the host for the expression of the transgene. The method
CC of the invention is designed to target mutation-driven non-self
CC determinants. The cellular immunogens induce reactivity for self-
CC determinants in the over expressed product of tumour associated and over
CC expressed proto-oncogenes
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 3; Length 4530;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4383 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 4442

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4443 GGGGAGAATGGGT 4455
```

RESULT 13
AAD19731
ID AAD19731 standard; cDNA; 4530 BP.
XX
AC AAD19731;
XX
DT 11-JUN-2007 (revised)
DT 18-DEC-2001 (first entry)
XX
DE Human tyrosine kinase-type receptor, HER-2 cDNA.
XX
KW Therapeutic compound; major histocompatibility complex; vaccine;
KW antigenic peptide; MHC; immunoregulatory; immune response; HER-2;
KW adoptive immunotherapy; anti-cancer; breast cancer antigen; APC;
KW antigen presenting cell; human; tyrosine kinase-type receptor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

```
FT   CDS             151. .3198
FT                   /*tag=  a
FT                   /product= "Human tyrosine kinase-type receptor, HER-2"
XX
PN   WO200168677-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-US040328.
XX
PR   16-MAR-2000; 2000US-00527487.
XX
PA   (GENZ ) GENZYME CORP.
XX
PI   Nicolette CA;
XX
DR   WPI; 2001-616284/71.
DR   P-PSDB; AAE12130.
DR   PC:NCBI; gi183986.
DR   PC_ENCPRO:NCBI; gi306840.
XX
PT   Novel synthetic therapeutic compound for inducing immune response and for
PT   use in adoptive immunotherapy, has enhanced binding to major
PT   histocompatibility molecules and enhanced immunoregulatory properties.
XX
PS   Disclosure; Page 57-63; 69pp; English.
XX
CC   The invention relates to synthetic therapeutic compounds (antigenic
CC   peptides) with enhanced binding to major histocompatibility complex (MHC)
CC   molecules and enhanced immunoregulatory properties relative to their
CC   natural counterparts. Compounds of the invention are useful for inducing
CC   an immune response in a subject and for use in adoptive immunotherapy.
CC   They are useful as components of anti-cancer vaccines and to expand
CC   immune effector cells that are specific for cancers characterised by
CC   expression of the breast cancer antigen, HER-2. Polynucleotides that
CC   encode peptides of the invention are useful as hybridisation probes and
CC   as primers for the detection of genes of gene transcripts that are
CC   expressed in antigen presenting cells (APCs), to confirm transduction of
CC   polynucleotides into host cells. The present sequence is human tyrosine
CC   kinase-type receptor, HER-2 cDNA
CC
CC   Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 73;  DB 5;  Length 4530;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-07;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4383 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 4442

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4443 GGGGAGAATGGGT 4455
```

RESULT 14
ABK83918
ID   ABK83918 standard; cDNA; 4530 BP.
XX
AC   ABK83918;
XX
DT   11-JUN-2007 (revised)
DT   14-AUG-2002 (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #489.
XX
KW   Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW   viral infection; parasitic infection; protozoal infection;
KW   fungal infection; sterile inflammatory disease; psoriasis;
KW   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW   cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW   adult respiratory distress syndrome; inflammatory bowel disease;
KW   Crohn's disease; ulcerative colitis; periodontal disease;
KW   granulocyte activation; chronic inflammation; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200228999-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US030821.
XX
PR   03-OCT-2000; 2000US-0237189P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR   WPI; 2002-435328/46.
DR   PC:NCBI; gi183986.
DR   PC_ENCPRO:NCBI; gi306840.
XX
PT   Detecting granulocyte activation by detecting differential expression of

PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX
PS Claim 1; SEQ ID NO 489; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
CC Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 6; Length 4530;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4383 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 4442

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4443 GGGGAGAATGGGT 4455
```

RESULT 15
ABN85585
ID   ABN85585 standard; DNA; 4530 BP.
XX
AC   ABN85585;
XX
DT   11-JUN-2007 (revised)
DT   09-SEP-2002 (first entry)
XX
DE   Human HER2-neu SEQ ID NO 11.
XX
KW   Human; EGFR; HER2-neu; chemotherapeutic regimen; tumour; cancer;
KW   receptor tyrosine kinase; epidermal growth factor receptor;
KW   gene expression; ds.
XX
OS   Homo sapiens.
XX
PN   WO200244413-A2.
XX
PD   06-JUN-2002.
XX
PF   09-NOV-2001; 2001WO-US043035.
XX
PR   01-DEC-2000; 2000US-0250122P.
PR   04-DEC-2000; 2000US-0250469P.
PR   11-JUN-2001; 2001US-00877177.
XX
PA   (RESP-) RESPONSE GENETICS INC.
XX
PI   Danenberg KD;
XX
DR   WPI; 2002-537460/57.
DR   PC:NCBI; gi183986.
DR   PC_ENCPRO:NCBI; gi306840.
XX
PT   Determining chemotherapeutic regimen of receptor tyrosine kinase targeted
PT   agent for treating tumor by examining EGFR and/or HER2-neu mRNA amount in
PT   tumor cells, comparing it to predetermined threshold expression level.
XX

```
PS   Disclosure; Page 124-125; 125pp; English.
XX
CC   The invention relates to determining the chemotherapeutic regimen of
CC   receptor tyrosine kinase targeted agent for treating tumour by amplifying
CC   mRNA from tumour and non-malignant tissues using a primer pair that
CC   hybridises to epidermal growth factor receptor (EGFR) and/or HER2-neu
CC   gene (I), quantitating and obtaining differential expression levels of
CC   amplified mRNA and comparing the differential expression levels and
CC   threshold levels for expression of (I). The method is useful for
CC   assessment of clinical treatment of a patient and as a diagnostic or
CC   prognostic tool for a range of cancers including breast, head and neck,
CC   lung, oesophageal and colorectal cancer. The present sequence is that of
CC   the human HER2-neu DNA sequence used in methods of the invention
CC
CC   Revised record issued on 11-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 73;  DB 6;  Length 4530;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-07;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4383 CTTTTCTGTTTAGTTTTTACTTTTTTTGTTTTGTTTTTTTTAAAGACGAAATAAAGACCCA 4442

Qy         61 GGGGAGAATGGGT 73
              |||||||||||||
Db       4443 GGGGAGAATGGGT 4455


Search completed: June  7, 2008, 14:10:25
Job time : 889 secs
```

SCORE 3 0